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RAW SEQUENCE LISTING

DATE: 04/16/2002

PATENT APPLICATION: US/10/029,890

TIME: 16:08:03

Input Set : N:\Crf3\RULE60\10029890.raw

Output Set: N:\CRF3\04162002\J029890.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
4 (i) APPLICANT: Soos, Jeanne M.
5 Schiffenbauer, Joel
6 Johnson, Howard M.
8 (ii) TITLE OF INVENTION: Orally-Administered Interferon-Tau
9 Compositions and Methods
11 (iii) NUMBER OF SEQUENCES: 6
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Dehlinger & Associates
15 (B) STREET: 350 Cambridge Ave., Suite 250
16 (C) CITY: Palo Alto
17 (D) STATE: CA
18 (E) COUNTRY: USA
19 (F) ZIP: 94306
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/10/029,890
C--> 29 (B) FILING DATE: 21-Dec-2001
30 (C) CLASSIFICATION:
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: US/08/616,904
35 (B) FILING DATE: 15-MAR-1996
38 (viii) ATTORNEY/AGENT INFORMATION:
39 (A) NAME: Sholtz, Charles K.
40 (B) REGISTRATION NUMBER: 38,615
41 (C) REFERENCE/DOCKET NUMBER: 5600-0003
43 (ix) TELECOMMUNICATION INFORMATION:
44 (A) TELEPHONE: 415-324-0880
45 (B) TELEFAX: 415-324-0960
47 (2) INFORMATION FOR SEQ ID NO: 1:
49 (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 516 base pairs
51 (B) TYPE: nucleic acid
52 (C) STRANDEDNESS: double
53 (D) TOPOLOGY: circular
W--> 55 (ii) MOLECULE TYPE: DNA
57 (iii) HYPOTHETICAL: NO
W--> 85 (iv) ANTI-SENSE: Purification and Antiviral Activity

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61      (vi) ORIGINAL SOURCE:
62          (A) ORGANISM: Ovis aries
63          (B) STRAIN: Domestic
64          (D) DEVELOPMENTAL STAGE: Blastula (blastocyst)
65          (F) TISSUE TYPE: Trophectoderm
66          (G) CELL TYPE: Mononuclear trophectoderm cells
67      (vii) IMMEDIATE SOURCE:
C--> 82          (B) CLONE: Cloning and Expression in Saccharomyces
83                  cerevisiae of a Synthetic Gene for the Type I
84                  Trophoblast Interferon Ovine Trophoblast
71      (viii) POSITION IN GENOME:
72          (C) UNITS: bp
74          (ix) FEATURE:
75              (A) NAME/KEY: CDS
76              (B) LOCATION: 1..516
77          (x) PUBLICATION INFORMATION:
78              (A) AUTHORS: Ott, Troy L
79              Van Heeke, Gino
80              Johnson, Howard M
81              Bazer, Fuller W
92          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
94      TGC TAC CTG TCG CGA AAA CTG ATG CTG GAC GCT CGA GAA AAT TTA AAA      48
95      Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys
96      1          5          10          15
98      CTG CTG GAC CGT ATG AAT CGA TTG TCT CCG CAC AGC TGC CTG CAA GAC      96
99      Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp
100     20          25          30
102     CGG AAA GAC TTC GGT CTG CCG CAG GAA ATG GTT GAA GGT GAC CAA CTG      144
103     Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu
104     35          40          45
106     CAA AAA GAC CAA GCT TTC CCG GTA CTG TAT GAA ATG CTG CAG CAG TCT      192
107     Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser
108     50          55          60
110     TTC AAC CTG TTC TAC ACT GAA CAT TCT TCG GCC GCT TGG GAC ACT ACT      240
111     Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
112     65          70          75          80
114     CTT CTA GAA CAA CTG TGC ACT GGT CTG CAA CAG CAA CTG GAC CAT CTG      288
115     Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Leu Asp His Leu
116     85          90          95
118     GAC ACT TGC CGT GGC CAG GTT ATG GGT GAA GAA GAC TCT GAA CTG GGT      336
119     Asp Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly
120     100         105         110
122     AAC ATG GAT CCG ATC GTT ACT GTT AAA AAA TAT TTC CAG GGT ATC TAC      384
123     Asn Met Asp Pro Ile Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr
124     115         120         125
126     GAC TAC CTG CAG GAA AAA GGT TAC TCT GAC TGC GCT TGG GAA ATC GTA      432
127     Asp Tyr Leu Gln Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val
128     130         135         140
130     CGC GTT GAA ATG ATG CGG GCC CTG ACT GTG TCG ACT ACT CTG CAA AAA      480

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131 Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys
132 145                      150                      155                      160
134 CGG TTA ACT AAA ATG GGT GGT GAC CTG AAT TCT CCG
135 Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro
136                      165                      170
138 (2) INFORMATION FOR SEQ ID NO: 2:
140 (i) SEQUENCE CHARACTERISTICS:
141 (A) LENGTH: 172 amino acids
142 (B) TYPE: amino acid
143 (D) TOPOLOGY: linear
145 (ii) MOLECULE TYPE: protein
147 (vi) ORIGINAL SOURCE:
148 (C) INDIVIDUAL ISOLATE: amino acid sequence of a mature
149 OvIFNtau protein
151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
153 Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys
154 1. 5 10 15
156 Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp
157 20 25 30
159 Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu
160 35 40 45
162 Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser
163 50 55 60
165 Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
166 65 70 75 80
168 Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu
169 85 90 95
171 Asp Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly
172 100 105 110
174 Asn Met Asp Pro Ile Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr
175 115 120 125
177 Asp Tyr Leu Gln Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val
178 130 135 140
180 Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys
181 145 150 155 160
183 Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro
184 165 170
187 (2) INFORMATION FOR SEQ ID NO: 3:
189 (i) SEQUENCE CHARACTERISTICS:
190 (A) LENGTH: 516 base pairs
191 (B) TYPE: nucleic acid
192 (C) STRANDEDNESS: single
193 (D) TOPOLOGY: linear
195 (ii) MOLECULE TYPE: cDNA
197 (vi) ORIGINAL SOURCE:
198 (C) INDIVIDUAL ISOLATE: synthetic nucleotide sequence encoding
199 a mature human interferon-tau protein, HuIFNtau1.
201 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
203 TGTGACTTGT CTCAAACCA CGTTTTGGTT GGTAGAAAGA ACTTAAGACT ACTAGACGAA 60

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205 ATGAGACGTC TATCTCCACG CTTCTGTCTA CAAGACAGAA AGGACTTCGC TTTGCCTCAG      120
207 GAAATGGTTG AAGGTGGCCA ACTACAAGAA GCTCAAGCGA TATCTGTTTT GCACGAAATG      180
209 TTGCAACAAA GCTTCAACTT GTTCCACACC GAACACTCTT CGGCCGCTTG GGACACCACC      240
211 TTGTTGGAAC AGCTCAGAAC CGGTTTGCAC CAACAATTGG ACAACTTGGA TGCATGTTTG      300
213 GGTCAAGTTA TGGGTGAAGA AGACTCTGCT CTCGGGAGAA CCGGTCCAAC GCTAGCTTTG      360
215 AAGAGATACT TCCAAGGTAT CCACGTTTAC TTGAAGGAAA AGGGTTACTC TGACTGTGCT      420
217 TGGGAAACCG TGCGTCTAGA AATCATGCGT AGCTTCTCTT CTTTGATCAG CTTGCAAGAA      480
219 AGATTACGTA TGATGGACGG TGACTTGTCG AGCCCA                                     516

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221 (2) INFORMATION FOR SEQ ID NO: 4:

223 (i) SEQUENCE CHARACTERISTICS:

224 (A) LENGTH: 172 amino acids

225 (B) TYPE: amino acid

226 (C) STRANDEDNESS: single

227 (D) TOPOLOGY: linear

229 (ii) MOLECULE TYPE: protein

231 (vi) ORIGINAL SOURCE:

232 (C) INDIVIDUAL ISOLATE: amino acid sequence for a mature
 233 HuIFNtau protein, HuIFNtau1.

235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

237 Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Arg Lys Asn Leu Arg
238 1      5      10      15
240 Leu Leu Asp Glu Met Arg Arg Leu Ser Pro Arg Phe Cys Leu Gln Asp
241      20      25      30
243 Arg Lys Asp Phe Ala Leu Pro Gln Glu Met Val Glu Gly Gly Gln Leu
244      35      40      45
246 Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser
247      50      55      60
249 Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
250      65      70      75      80
252 Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asn Leu
253      85      90      95
255 Asp Ala Cys Leu Gly Gln Val Met Gly Glu Glu Asp Ser Ala Leu Gly
256      100     105     110
258 Arg Thr Gly Pro Thr Leu Ala Leu Lys Arg Tyr Phe Gln Gly Ile His
259      115     120     125
261 Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Thr Val
262      130     135     140
264 Arg Leu Glu Ile Met Arg Ser Phe Ser Ser Leu Ile Ser Leu Gln Glu
265      145     150     155     160
267 Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro
268      165     170

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270 (2) INFORMATION FOR SEQ ID NO: 5:

272 (i) SEQUENCE CHARACTERISTICS:

273 (A) LENGTH: 516 base pairs

274 (B) TYPE: nucleic acid

275 (C) STRANDEDNESS: double

276 (D) TOPOLOGY: linear

278 (ii) MOLECULE TYPE: DNA (genomic)

280 (iii) HYPOTHETICAL: NO

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TIME: 16:08:03

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282      (iv) ANTI-SENSE: NO
284      (vi) ORIGINAL SOURCE:
285          (C) INDIVIDUAL ISOLATE: HuIFNtau3, mature no leader sequence
287      (ix) FEATURE:
288          (A) NAME/KEY: CDS
289          (B) LOCATION: 1..516
291      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
293 TGT GAC CTG TCT CAG AAC CAC GTG CTG GTT GGC AGC CAG AAC CTC AGG      48
294 Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg
295   1           5           10           15
297 CTC CTG GGC CAA ATG AGG AGA CTC TCC CTT CGC TTC TGT CTG CAG GAC      96
298 Leu Leu Gly Gln Met Arg Arg Leu Ser Leu Arg Phe Cys Leu Gln Asp
299           20           25           30
301 AGA AAA GAC TTC GCT TTC CCC CAG GAG ATG GTG GAG GGT GGC CAG CTC      144
302 Arg Lys Asp Phe Ala Phe Pro Gln Glu Met Val Glu Gly Gly Gln Leu
303           35           40           45
305 CAG GAG GCC CAG GCC ATC TCT GTG CTC CAC GAG ATG CTC CAG CAG AGC      192
306 Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser
307           50           55           60
309 TTC AAC CTC TTC CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC      240
310 Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
311   65           70           75           80
313 CTC CTG GAG CAG CTC CGC ACT GGA CTC CAT CAG CAG CTG GAT GAC CTG      288
314 Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asp Leu
315           85           90           95
317 GAT GCC TGC CTG GGG CAG GTG ACG GGA GAG GAA GAC TCT GCC CTG GGA      336
318 Asp Ala Cys Leu Gly Gln Val Thr Gly Glu Glu Asp Ser Ala Leu Gly
319           100          105          110
321 AGA ACG GGC CCC ACC CTG GCC ATG AAG AGG TAT TTC CAG GGC ATC CAT      384
322 Arg Thr Gly Pro Thr Leu Ala Met Lys Arg Tyr Phe Gln Gly Ile His
323           115          120          125
325 GTC TAC CTG AAA GAG AAG GGA TAT AGT GAC TGC GCC TGG GAA ATT GTC      432
326 Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val
327           130          135          140
329 AGA CTG GAA ATC ATG AGA TCC TTG TCT TCA TCA ACC AGC TTG CAC AAA      480
330 Arg Leu Glu Ile Met Arg Ser Leu Ser Ser Ser Thr Ser Leu His Lys
331 145           150          155          160
333 AGG TTA AGA ATG ATG GAT GGA GAC CTG AGC TCA CCT      516
334 Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro
335           165          170
338 (2) INFORMATION FOR SEQ ID NO: 6:
340      (i) SEQUENCE CHARACTERISTICS:
341          (A) LENGTH: 172 amino acids
342          (B) TYPE: amino acid
343          (D) TOPOLOGY: linear
345      (ii) MOLECULE TYPE: protein
347      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
349 Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg
350   1           5           10           15

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VERIFICATION SUMMARY

DATE: 04/16/2002

PATENT APPLICATION: US/10/029,890

TIME: 16:08:04

Input Set : N:\CrF3\RULE60\10029890.raw

Output Set: N:\CRF3\04162002\J029890.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:82 M:220 C: Keyword misspelled or invalid format, [(B) CLONE:]
L:85 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:55 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:85 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=1